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<110> Max-Planck-Gesellschaft z.
Förd. d. Wissenschaften

<120> Plants With Modified Gene Expression

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<140> 10/030,386

<140> 2002-01-02

<150> PCT/DE00/02233

<151> 2000-07-03

<150> DE 199 30 570.6

<151> 1999-07-02

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<170> PatentIn Ver. 2.1

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 Asp Arg Ile Asn Leu Asn Ser Asn Leu Asp Leu Asn Pro Asn Pro Leu
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 65 70 75 80
 Arg Glu Val Asp Val Asp Leu His Ile Gly Leu Pro Gly Phe Gly Lys
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<213> *Arabidopsis thaliana*

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Peptide

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Leu	Pro	Pro	Val	Thr	Pro	Pro	Ser	Ser	Phe	Phe	Phe	Phe	Pro	Gln	Ser	35	40	45	
Gly	Asp	Leu	Arg	Arg	Pro	Pro	Pro	Pro	Thr	Pro	Pro	Pro	Ser	Pro		50	55	60	
Pro	Leu	Arg	Glu	Ala	Leu	Pro	Leu	Leu	Ser	Leu	Ser	Pro	Ala	Asn	Lys	65	70	75	80
Gln	Gln	Asp	His	His	His	Asn	His	Asp	His	Leu	Ile	Gln	Glu	Pro	Pro	85	90	95	
Ser	Thr	Ser	Met	Asp	Val	Asp	Tyr	Asp	His	His	His	Gln	Asp	Asp	His	100	105	110	
His	Asn	Leu	Asp	Asp	Asp	Asp	His	Asp	Val	Thr	Val	Ala	Leu	His	Ile	115	120	125	
Gly	Leu	Pro	Ser	Pro	Ser	Ala	Gln	Glu	Met	Ala	Ser	Leu	Leu	Met	Met	130	135	140	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Arg	Thr	Thr	His	His	His	Glu	Asp	Met	145	150	155	160
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Gln	Ile	Leu	Ile	Gly	Pro	Thr	Gln	Phe	Ser	Cys	Pro	Val	Cys	Phe	Lys	210	215	220	
Thr	Phe	Asn	Arg	Tyr	Asn	Asn	Met	Gln	Met	His	Met	Trp	Gly	His	Gly	225	230	235	240
Ser	Gln	Tyr	Arg	Lys	Gly	Pro	Glu	Ser	Leu	Arg	Gly	Thr	Gln	Pro	Thr	245	250	255	
Gly	Met	Leu	Arg	Leu	Pro	Cys	Tyr	Cys	Cys	Ala	Pro	Gly	Cys	Arg	Asn	260	265	270	
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Gly	Ala	Tyr	Gly	Ile	Asp	Gly	Phe	Asp	Glu	Glu	Asp	Glu	Pro	Ala	Ser		
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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

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Tyr	Leu	Ala	Phe	Thr	Gly	Phe	Leu	Thr	Gln	Leu	His	His	Leu	Glu	Ile
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Ser	Cys	Leu	Leu	Leu	Leu	Phe	Phe	Ser	Leu	Ser	Ser	Leu	Leu	Lys	Leu
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65					70					75				80	
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				85					90					95	
His	Asp	Ser	Phe	Phe	Phe	Phe	Pro	Gln	Ser	Gly	Asp	Leu	Arg	Arg	Pro
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Pro	Pro	Pro	Pro	Thr	Pro	Pro	Pro	Ser	Pro	Pro	Leu	Arg	Glu	Ala	Leu
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Pro Leu Leu Ser Leu Ser Pro Ala Asn Thr Gln Gln Asp His His His
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 145 150 155 160
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 165 170 175
 Asp His Asp Val Thr Val Ala Leu His Ile Gly Leu Pro Ser Pro Ser
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 Ala Gln Glu Met Ala Ser Leu Leu Met Met Ser Ser Ser Ser Ser Ser
 195 200 205
 Ser Arg Thr Thr His His His Glu Asp Met Asn His Lys Lys Asp Leu
 210 215 220
 Asp His Glu Tyr Ser His Gly Ala Val Gly Gly Gly Glu Asp Asp Asp
 225 230 235 240
 Glu Asp Ser Val Gly Gly Asp Gly Gly Cys Arg Ile Ser Arg Leu Asn
 245 250 255
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 260 265 270
 Thr Gln Phe Ser Cys Pro Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn
 275 280 285
 Asn Met Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly
 290 295 300
 Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr Gly Met Leu Arg Leu Pro
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 Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn Asn Ile Asp His Pro Arg
 325 330 335
 Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg
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 Lys His Gly Ile Lys Pro Phe Met Cys Arg Lys Cys Gly Lys Ala Phe
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 Ala Val Arg Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Leu
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 Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys
 385 390 395 400
 Asp His Ile Lys Ala Phe Thr Asn Gly His Gly Ala Tyr Gly Ile Asp
 405 410 415
 Gly Phe Asp Glu Glu Asp Glu Pro Ala Ser Glu Val Glu Gln Leu Asp

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic Peptide

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 Leu Pro Leu Leu Ser Leu Ser Pro Ile Arg His Gln Glu Gln Gln Asp
 65 70 75 80
 Gln His Tyr Phe Met Asp Thr His Gln Ile Ser Ser Ser Asn Phe Leu
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 Asp Glu Gln Asp Gln Asp His Asp Arg Gly Val Glu Val Thr Val Glu
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 Ser His Leu Asp Asp Asp Asp Asp His His Gly Asp Leu His Arg Gly
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 His His Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro Thr
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Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His Gly Ser Lys Pro Phe
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Ala Cys Arg Met Cys Gly Lys Ala Phe Ala Val Lys Gly Asp Trp Arg
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Thr His Glu Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ser Cys Gly Ser
 245 250 255

Asp Phe Lys His Lys Arg Ser Leu Lys Asp His Val Lys Ala Phe Gly
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<210> 8

<211> 54

<212> PRT

<213> Artificial Sequence

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 Peptide

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Leu Lys Asp Phe Arg Thr
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51	ACCTAGACACCATTTCGAATCCCTTGATCTCTTCCCTAACCTCAACAAA	100
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1111	gcacatgtggggacatggttcacaatacaggaaaggaccggagtcactga	1160
486	GCACATGTGGGGACATGGTTCACAATACAGGAAAGGACCGGAGTCACTGA	535
1161	aaggcacacagccacgagccatggttagggatcccttggtactgctgcgtt	1210
536	AAGGCACACAGCCACGAGCCATGTTAGGGATCCCTTGTTACTGCTGCGTT	585
1211	gaaggggtgcaggaaccacattgaccatcctcggttccaagccactgaaaga	1260
586	GAAGGGTGCAGGAACCACATTGACCATCCTCGTTCCAAGCCACTGAAAGA	635
1261	ctttaggacgctccaaacgcactacaaacgcaaacacggacacaaaccct	1310
636	CTTTAGGACGCTCCAAACGCACTACAAACGCAAACACGGACACAAACCCT	685
1311	tctcgtgtcgcctttgcggttaagcttttggctgtcaagggcgattggcga	1360
686	TCTCGTGTGCGCTTTGCGGTAAGCTTTTGGCTGTCAAGGGCGATTGGCGA	735
1361	acacatgagaagaattgtggaacacgttggtttgctgttgcggttctga	1410



SEQ2-4align_051124MS.txt

```

56 ACACATGAGAAGAATTGTGGAAAACGTTGGGTTTGC GTTTGCGGTTCTGA 785
1411 ttttaaacacaaacgttctcttaaggaccatgttaaggcgtttgggtctg 1460
786 TTTTAAACACAAACGTTCTCTTAAGGACCATGTTAAGGCGTTTGGGTCTG 835
1461 gtcatggggccttatccaactggtttgtttgaagagcaggcttctaattca 1510
836 GTCATGGGCCTTATCCAAC TGGTTTGT TTGAAGAGCAGGCTTCTAATTCA 885
1511 tctgtctccgagactttgttttttaaat tgg.....agctt 1816
886 TCTGTCTCCGAGACTTTGTTTTTTTAA >>>> 279 >>>> \ 912

```

Note Best alignment is between forward est and forward genome, and splice sites imply forward gene

Exon	483	100.0	1	483	1	483
+Intron	-20	0.0	484	1108		
Exon	429	100.0	1109	1537	484	912
Span	892	100.0	1	1537	1	912
Segment	483	100.0	1	483	1	483
Segment	429	100.0	1109	1537	484	912

Alignment Score: 892